AMENDMENTS TO THE CLAIMS:

Amend the claims as follows:

1. (Original) An isolated nucleic acid molecule consisting of SEQ ID NO 1, its complementary form, or RNA form thereof.

2. (Original) An isolated nucleic acid molecule consisting of SEQ ID NO 2, its complementary form, or RNA form thereof.

3. (Currently Amended) An isolated nucleic acid molecule that specifically hybridizes to SEQ ID NO 1 [[or 2]], or to the RNA form of said SEQ ID NO 1 [[or 2]] wherein T is replaced by U, or to the complementary form of said SEQ ID NO 1[[or 2]], or to a fragment of at least 20 contiguous nucleotides thereof, or to any of their homologues, for the detection and/or identification of Staphylococcus species, in particular of S. aureus.

4. (Currently Amended) An isolated nucleic acid molecule according to claim 3 or claim 16, consisting of a nucleic acid selected from the group consisting of SEQ IDs NO 14, 16 to 23, 25 to 32, 35 to 42, 51, 52, 53, 55, 58, 65, 67, 68, 69 and 70.

5. (Original) A set of two polynucleotide probes, said two probes hybridizing specifically to SEQ ID NO 1 or SEQ ID NO 2 or homologues, or to their RNA form wherein T is replaced by U, or to their complementary form, wherein there are no more than 25 nucleotides between said two probes.

6. (Original) A set of two polynucleotide probes according to claim 5 consisting of SEQ IDs NO 15 and 20, or SEQ IDs NO 15 and 21, or SEQ IDs NO 17 and 16, or SEQ IDs NO 17 and 19, or SEQ IDs NO 26 and 14, or SEQ IDs NO 27 and 28, or SEQ IDs NO 29 and 22, or SEQ IDs NO 32 and 39, or SEQ IDs NO 32 and 23, or SEQ IDs

NO 30 and 18, or SEQ IDs NO 36 and 38, or SEQ IDs NO 37 and 35, or SEQ IDs NO 40 and 25, or SEQ IDs NO 41 and 31, or SEQ IDs NO 42 and 43.

7. (Previously Presented) A composition comprising at least one nucleic acid molecule according to claim 1 and/or a set of two polynucleotide probes hybridizing specifically to SEQ ID NO 1 or SEQ ID NO 2 or homologues, or to their RNA form wherein T is replaced by U, or to their complementary form, wherein there are no more than 25 nucleotides between said two probes.

8. (Currently Amended) A method for the detection and/or identification of Staphylococcus species, in particular S. aureus, ,using a nucleic acid molecule as defined in claim 1 or 2 wherein in the RNA form T is replaced by U or a fragment of at least 20 contiguous nucleotides thereof, or any of their homologues ~~Use of a nucleic acid molecule consisting of SEQ ID NO 1 or 2, or of the RNA form of said SEQ ID NO 1 or 2 wherein T is replaced by U, or of the complementary form of said SEQ ID NO 1or 2, or of a fragment of at least 20 contiguous nucleotides thereof, or of any of their homologues, for the detection and/or identification of Staphylococcus species, in particular of S. aureus~~.

9. (Previously Presented) A method for detecting or identifying Staphylococcus species using at least one nucleic acid molecule according to claim 1.

10. (Original) A method according to claim 9 for detection and/or identification of Staphylococcus species in a sample comprising the steps of:

(i) if need be releasing, isolating and/or concentrating the polynucleic acids in the sample;

(ii) if need be amplifying the 16S-23S rRNA spacer region, or a fragment comprising the target sequence, or the target sequence or a fragment thereof, with at least one suitable primer pair;

(iii) hybridizing the polynucleic acids of step (i) or (ii) with at least one polynucleotide probe that hybridizes to the target sequence,

wherein the target sequence of step (ii) and (iii) consists of SEQ ID NO 1 or 2 or homologues thereof, or to their RNA form wherein T is replaced by U, or to their complementary form, or a to a fragment of at least 20 contiguous nucleotides thereof,

(iv) detecting the hybrids formed, and

(v) interpreting the signal(s) obtained and inferring the presence of Staphylococcus species and/or identifying the Staphylococcus species in the sample.

11. (Original) A method according to claim 10 wherein a suitable primer pair consists of any combination of a forward primer polynucleotide selected from the group consisting of SEQ ID NO 45, 49, 50, 52, 56, 61, 63, 64, 65, 66, 67, 68 and their homologues, and a reverse primer polynucleotide selected from the group consisting of SEQ ID NO 46, 47, 48, 51, 53, 54, 55, 57, 58, 59, 60, 62, and their homologues.

12. (Previously Presented) A method according to claim 10 wherein two polynucleotide probes are used.

13. (Original) A method according to claim 12 wherein the two polynucleotide probes hybridize to the target sequence adjacent to each other with less than 25 nucleotides in between.

14. (Original) A method according to claim 13 wherein the two polynucleotide probes consist of polynucleotides of SEQ IDs NO 15 and 20, or 15 and 21, or 17 and

16, or 17 and 19, or 26 and 14, or 27 and 28, or 29 and 22, or 32 and 39, or 32 and 23, or 30 and 18, or 36 and 38, or 37 and 35, or 40 and 25, or 41 and 31, or 42 and 43.

15. (Previously Presented) A kit for detection and/or identification of Staphylococcus species comprising the following components:

- at least one nucleic acid molecule according to claim 1 and/or a set of two polynucleotide probes hybridizing specifically to SEQ ID NO 1 or SEQ ID NO 2 or homologues, or to their RNA form wherein T is replaced by U, or to their complementary form, wherein there are no more than 25 nucleotides between said two probes.

- a hybridization buffer, or components necessary for producing said buffer.

16. (new) An isolated nucleic acid molecule of at most 100 contiguous nucleotides that specifically hybridizes to SEQ ID NO 2, or to the RNA form of said SEQ ID NO 2 wherein T is replaced by U, or to the complementary form of said SEQ ID NO 2, or to a fragment of at least 20 contiguous nucleotides thereof, or to any of their homologues, for the detection and/or identification of Staphylococcus species, in particular of S. aureus.